

**Amendment to the Specification:**

Replace the paragraph beginning at page 34, line 5, with the following amended paragraph:

In order to confirm the presence of a full-length Ly111b transcript in the human brain, a PCR was performed from complementary DNA taken from human fetal brain (Marathon Ready cDNA, Clontech), using the oligonucleotides LyF1 (AAT GGA AGG GCG TGA CGC, Figure 5, SEQ ID NO: 38) and HA71 (CCT CAC GCC TGC TGC AAC CTG, SEQ ID NO: 39) as primers. A DNA fragment with low representation of approximately two kilobases was amplified. The product of this first PCR served as a matrix for a nested PCR, carried out with oligonucleotides LyEcoF (GCACGAATTC ATG GCC CAA GAA ATA GAT CTG, SEQ ID NO: ~~[[41]]~~ 40) and HA72 (CTG TCT TCG TAT TTC TCC GCC TTG, SEQ ID NO: 41). The amplified products were digested with the restriction enzymes EcoRI (integrated into the oligonucleotide LyEcoF) and BstEII (Figure 5) and inserted into the expression vector pcDNA3, then their sequence was determined. Analysis of the clone sequences obtained revealed the presence of two potential full-length Ly111b transcripts in the human fetal brain (Figure 5). The first of these transcripts (Ly111b<sub>fullA</sub>) corresponds to the mRNA which was identified in the human lung (Example 6) and encodes a 609 amino acid protein (pLy111b<sub>fullA</sub>; Figures 5, 6). The second (LY111b<sub>fullB</sub>) probably represents an alternative splicing product of a common primary mRNA. In this transcript, which is identical to LY111b<sub>fullA</sub>, the sequence between the nucleotides 752 and 956 of the sequence validated in the human lung is absent. LY111b<sub>fullB</sub> thus encodes a 541 amino acid protein (pLY111b<sub>fullB</sub>) (SEQ ID NO: 50) which is identical to pLY111b<sub>fullA</sub> (SEQ ID NO: 48), in which, however, the domain included between amino acids 172 and 240 (Figures 5, 7) is missing. The two proteins pLY111b<sub>fullA/fullB</sub> integrate into the domain of interaction with the fragment of parkin which comprises amino acids 135 to 290, which were identified in the yeast (initial sequence, LY111b Figure 5), and can therefore theoretically maintain this interaction.